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Reviewer: markspencer

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Application No: 08422548 Version No: 2.0

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Eaton, Dan L.
de Sauvage, Frederic J.

(ii) TITLE OF INVENTION: HUMAN MPL LIGAND

(iii) NUMBER OF SEQUENCES: 30

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08422548
(B) FILING DATE: 2012-01-12
(A) APPLICATION NUMBER: 08422548
(B) FILING DATE: 2012-01-12
(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08223263
(B) FILING DATE: 1994-04-04

(vii) PRIOR APPLICATION DATA:

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(B) FILING DATE: 04-Apr-1994

(vii) PRIOR APPLICATION DATA:

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(B) FILING DATE: 15-FEB-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/185607
(B) FILING DATE: 21-JAN-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/176553
(B) FILING DATE: 3-JAN-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Winter, Daryl B.
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(C) REFERENCE/DOCKET NUMBER: P0871P3

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Glu	Leu	Thr	Glu	Leu	Leu	Leu	Val	Val	Met	Leu	Leu	Leu	Thr
-21	-20							-15						-10
Ala	Arg	Leu	Thr	Leu	Ser	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu
	-5						1				5			
Arg	Val	Leu	Ser	Lys	Leu	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser
10					15					20				
Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val
25					30					35				
Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln
40					45					50				
Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu
55					60					65				
Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr
70					75					80				
Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu
85					90					95				
Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro
100					105					110				
Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu
115					120					125				
Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu
130					135					140				
Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Arg	Ala	Pro	Pro	Thr	Thr
145					150					155				
Ala	Val	Pro	Ser	Arg	Thr	Ser	Leu	Val	Leu	Thr	Leu	Asn	Glu	Leu
160					165					170				

GTG GTC ATG CTT CTC CTA ACT GCA AGG CTA ACG CTG TCC 278
 Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu Ser
 -10 -5

AGC CCG GCT CCT CCT GCT TGT GAC CTC CGA GTC CTC AGT 317
 Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser
 1 5 10

AAA CTG CTT CGT GAC TCC CAT GTC CTT CAC AGC AGA CTG 356
 Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
 15 20 25

AGC CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA CCT GTC 395
 Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
 30 35

CTG CTG CCT GCT GTG GAC TTT AGC TTG GGA GAA TGG AAA 434
 Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys
 40 45 50

ACC CAG ATG GAG GAG ACC AAG GCA CAG GAC ATT CTG GGA 473
 Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly
 55 60 65

GCA GTG ACC CTT CTG CTG GAG GGA GTG ATG GCA GCA CGG 512
 Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg
 70 75

GGA CAA CTG GGA CCC ACT TGC CTC TCA TCC CTC CTG GGG 551
 Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly
 80 85 90

CAG CTT TCT GGA CAG GTC CGT CTC CTC CTT GGG GCC CTG 590
 Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu
 95 100

CAG AGC CTC CTT GGA ACC CAG CTT CCT CCA CAG GGC AGG 629
 Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg
 105 110 115

ACC ACA GCT CAC AAG GAT CCC AAT GCC ATC TTC CTG AGC 668
 Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu Ser
 120 125 130

TTC CAA CAC CTG CTC CGA GGA AAG GTG CGT TTC CTG ATG 707
 Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met
 135 140

CTT GTA GGA GGG TCC ACC CTC TGC GTC AGG CGG GCC CCA 746
 Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro
 145 150 155

CCC ACC ACA GCT GTC CCC AGC AGA ACC TCT CTA GTC CTC 785
 Pro Thr Thr Ala Val Pro Ser Arg Thr Ser Leu Val Leu
 160 165

ACA CTG AAC GAG CTC CCA AAC AGG ACT TCT GGA TTG TTG 824

Thr Leu Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu
170 175 180

GAG ACA AAC TTC ACT GCC TCA GCC AGA ACT ACT GGC TCT 863
Glu Thr Asn Phe Thr Ala Ser Ala Arg Thr Thr Gly Ser
185 190 195

GGG CTT CTG AAG TGG CAG CAG GGA TTC AGA GCC AAG ATT 902
Gly Leu Leu Lys Trp Gln Gln Gly Phe Arg Ala Lys Ile
200 205

CCT GGT CTG CTG AAC CAA ACC TCC AGG TCC CTG GAC CAA 941
Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu Asp Gln
210 215 220

ATC CCC GGA TAC CTG AAC AGG ATA CAC GAA CTC TTG AAT 980
Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn
225 230

GGA ACT CGT GGA CTC TTT CCT GGA CCC TCA CGC AGG ACC 1019
Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr
235 240 245

CTA GGA GCC CCG GAC ATT TCC TCA GGA ACA TCA GAC ACA 1058
Leu Gly Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr
250 255 260

GGC TCC CTG CCA CCC AAC CTC CAG CCT GGA TAT TCT CCT 1097
Gly Ser Leu Pro Pro Asn Leu Gln Pro Gly Tyr Ser Pro
265 270

TCC CCA ACC CAT CCT CCT ACT GGA CAG TAT ACG CTC TTC 1136
Ser Pro Thr His Pro Pro Thr Gly Gln Tyr Thr Leu Phe
275 280 285

CCT CTT CCA CCC ACC TTG CCC ACC CCT GTG GTC CAG CTC 1175
Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu
290 295

CAC CCC CTG CTT CCT GAC CCT TCT GCT CCA ACG CCC ACC 1214
His Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr
300 305 310

CCT ACC AGC CCT CTT CTA AAC ACA TCC TAC ACC CAC TCC 1253
Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His Ser
315 320 325

CAG AAT CTG TCT CAG GAA GGG T AAGGT TCTCAGACAC 1290
Gln Asn Leu Ser Gln Glu Gly
330 332

TGCCGACATC AGCATTGTCT CATGTACAGC TCCCTTCCCT GCAGGGCGCC 1340

CCTGGGAGAC AACTGGACAA GATTTCCTAC TTCTCTCTGA AACCCAAAGC 1390

CCTGGTAAAA GGGATACACA GGAATGAAAA GGGAATCATT TTCTACTGTA 1440

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CATTATAAAC CTTCAGAAGC TATTTTTTTTA AGCTATCAGC AATACTCATC 1490
AGAGCAGCTA GCTCTTTGGT CTATTTTCTG CAGAAATTTG CAACTCACTG 1540
ATTCTCTACA TGCTCTTTTT CTGTGATAAC TCTGCAAAGG CCTGGGCTGG 1590
CCTGGCAGTT GAACAGAGGG AGAGACTAAC CTTGAGTCAG AAAACAGAGA 1640
AAGGGTAATT TCCTTTGCTT CAAATTCAAG GCCTTCCAAC GCCCCCATCC 1690
CCTTTACTAT CATTCTCAGT GGGACTCTGA TCCCATATTC TTAACAGATC 1740
TTTACTCTTG AGAAATGAAT AAGCTTTCTC TCAGAAAAAA AAAAAAAAAA 1790
AAAAA 1795
```


5

10

15

GAC TCC CAT GTC CTT CAC AGC AGA CTG GTGA GAACTCCCAA 210

Asp Ser His Val Leu His Ser Arg Leu

20

25 26

CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA CTCCCAGGAA 260

GACACCATCA CTTCTCTAA CTCCTTGACC CAATGACTAT TCTTCCCATA 310

TTGTCCCCAC CTA CTGATCA CACTCTCTGA CAAGAATTAT TCTTCACAAT 360

ACAGCCCGCA TTTAAAAGCT CTCGTCTAGA 390

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 390 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCTAGACGAG AGCTTTTAAA TGCGGGCTGT ATTGTGAAGA ATAATTCTTG 50

TCAGAGAGTG TGATCAGTAG GTGGGGACAA TATGGGAAGA ATAGTCATTG 100

GGTCAAGGAG TTAGAGGAAG TGATGGTGTC TTCCTGGGAG TATGGGTGTC 150

TTACCAGTTA CGCGGATAAA GGGGATAATG TTGGGAGTTC TCACCAGTCT 200

GCTGTGAAGG ACATGGGAGT CACGAAGCAG TTTACTGAGG ACTCGGAGGT 250

CACAAGCAGG AGGAGCCGGG CTGGACAGCG TTAGCCTTGC AGTTAGGAGA 300

AGCATGACCA CGAGGAGCAA TTCTTAGATG AGGAGAGGTG AGGTTGAAAG 350

ATGAGGAGGA AATCATTGTC AGCTGGTATT CCAGGAATTC 390

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu

1

5

10

15

Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro

20

25

30

Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp

				35					40					45
Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala
				50					55					60
Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met
				65					70					75
Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu
				80					85					90
Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln
				95					100					105
Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala
				110					115					120
His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu
				125					130					135
Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu
				140					145					150
Cys	Val	Arg	Arg	Ala	Pro	Pro	Thr	Thr	Ala	Val	Pro	Ser	Arg	Thr
				155					160					165
Ser	Leu	Val	Leu	Thr	Leu	Asn	Glu	Leu	Pro	Asn	Arg	Thr	Ser	Gly
				170					175					180
Leu	Leu	Glu	Thr	Asn	Phe	Thr	Ala	Ser	Ala	Arg	Thr	Thr	Gly	Ser
				185					190					195
Gly	Leu	Leu	Lys	Trp	Gln	Gln	Gly	Phe	Arg	Ala	Lys	Ile	Pro	Gly
				200					205					210
Leu	Leu	Asn	Gln	Thr	Ser	Arg	Ser	Leu	Asp	Gln	Ile	Pro	Gly	Tyr
				215					220					225
Leu	Asn	Arg	Ile	His	Glu	Leu	Leu	Asn	Gly	Thr	Arg	Gly	Leu	Phe
				230					235					240
Pro	Gly	Pro	Ser	Arg	Arg	Thr	Leu	Gly	Ala	Pro	Asp	Ile	Ser	Ser
				245					250					255
Gly	Thr	Ser	Asp	Thr	Gly	Ser	Leu	Pro	Pro	Asn	Leu	Gln	Pro	Gly
				260					265					270
Tyr	Ser	Pro	Ser	Pro	Thr	His	Pro	Pro	Thr	Gly	Gln	Tyr	Thr	Leu
				275					280					285
Phe	Pro	Leu	Pro	Pro	Thr	Leu	Pro	Thr	Pro	Val	Val	Gln	Leu	His
				290					295					300
Pro	Leu	Leu	Pro	Asp	Pro	Ser	Ala	Pro	Thr	Pro	Thr	Pro	Thr	Ser
				305					310					315
Pro	Leu	Leu	Asn	Thr	Ser	Tyr	Thr	His	Ser	Gln	Asn	Leu	Ser	Gln

320

325

330

Glu Gly
332

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp	Ser	Arg	Val	Leu	Glu	Arg	Tyr	1	5	10	15
Leu	Leu	Glu	Ala	Lys	Glu	Ala	Glu	Asn	Ile	Thr	Thr	Gly	Cys	Ala	20	25	30	
Glu	His	Cys	Ser	Leu	Asn	Glu	Asn	Ile	Thr	Val	Pro	Asp	Thr	Lys	35	40	45	
Val	Asn	Phe	Tyr	Ala	Trp	Lys	Arg	Met	Glu	Val	Gly	Gln	Gln	Ala	50	55	60	
Val	Glu	Val	Trp	Gln	Gly	Leu	Ala	Leu	Leu	Ser	Glu	Ala	Val	Leu	65	70	75	
Arg	Gly	Gln	Ala	Leu	Leu	Val	Asn	Ser	Ser	Gln	Pro	Trp	Glu	Pro	80	85	90	
Leu	Gln	Leu	His	Val	Asp	Lys	Ala	Val	Ser	Gly	Leu	Arg	Ser	Leu	95	100	105	
Thr	Thr	Leu	Leu	Arg	Ala	Leu	Gly	Ala	Gln	Lys	Glu	Ala	Ile	Ser	110	115	120	
Pro	Pro	Asp	Ala	Ala	Ser	Ala	Ala	Pro	Leu	Arg	Thr	Ile	Thr	Ala	125	130	135	
Asp	Thr	Phe	Arg	Lys	Leu	Phe	Arg	Val	Tyr	Ser	Asn	Phe	Leu	Arg	140	145	150	
Gly	Lys	Leu	Lys	Leu	Tyr	Thr	Gly	Glu	Ala	Cys	Arg	Thr	Gly	Asp	155	160	165	
Arg															166			

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGTCCTTGG CCCACCTCTC TCCCACCCGA CTCTGCCGAA AGAAGCACAG 50

AAGCTCAAGC CGCCTCCATG GCCCCAGGAA AGATTCAGGG GAGAGGCCCC 100

ATACAGGGAG CCACTTCAGT TAGACACCCT GGCCAGA ATG GAG 143
Met Glu
-21 -20

CTG ACT GAT TTG CTC CTG GCG GCC ATG CTT CTT GCA GTG 182
Leu Thr Asp Leu Leu Leu Ala Ala Met Leu Leu Ala Val
-15 -10

GCA AGA CTA ACT CTG TCC AGC CCC GTA GCT CCT GCC TGT 221
Ala Arg Leu Thr Leu Ser Ser Pro Val Ala Pro Ala Cys
-5 1 5

GAC CCC AGA CTC CTA AAT AAA CTG CTG CGT GAC TCC CAC 260
Asp Pro Arg Leu Leu Asn Lys Leu Leu Arg Asp Ser His
10 15 20

CTC CTT CAC AGC CGA CTG AGT CAG TGT CCC GAC GTC GAC 299
Leu Leu His Ser Arg Leu Ser Gln Cys Pro Asp Val Asp
25 30

CCT TTG TCT ATC CCT GTT CTG CTG CCT GCT GTG GAC TTT 338
Pro Leu Ser Ile Pro Val Leu Leu Pro Ala Val Asp Phe
35 40 45

AGC CTG GGA GAA TGG AAA ACC CAG ACG GAA CAG AGC AAG 377
Ser Leu Gly Glu Trp Lys Thr Gln Thr Glu Gln Ser Lys
50 55

GCA CAG GAC ATT CTA GGG GCA GTG TCC CTT CTA CTG GAG 416
Ala Gln Asp Ile Leu Gly Ala Val Ser Leu Leu Leu Glu
60 65 70

GGA GTG ATG GCA GCA CGA GGA CAG TTG GAA CCC TCC TGC 455
Gly Val Met Ala Ala Arg Gly Gln Leu Glu Pro Ser Cys
75 80 85

CTC TCA TCC CTC CTG GGA CAG CTT TCT GGG CAG GTT CGC 494
Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg
90 95

CTC CTC TTG GGG GCC CTG CAG GGC CTC CTA GGA ACC CAG 533
Leu Leu Leu Gly Ala Leu Gln Gly Leu Leu Gly Thr Gln
100 105 110

GGC AGG ACC ACA GCT CAC AAG GAC CCC AAT GCC CTC TTC 572
Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Leu Phe
115 120

TTG AGC TTG CAA CAA CTG CTT CGG GGA AAG GTG CGC TTC 611

Leu Ser Leu Gln Gln Leu Leu Arg Gly Lys Val Arg Phe
125 130 135